

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/013,895DATE: 02/25/98
TIME: 13:56:30

INPUT SET: S23809.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: NI, JIAN
ROSEN, CRAIG A.
PAN, JAMES G.
GENTZ, REINER L.
DIXIT, VISHVA M.

ENTERED

(ii) TITLE OF INVENTION: Death Domain Containing Receptor-4

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: HUMAN GENOME SCIENCES, INC.
(B) STREET: 9410 KEY WEST AVENUE
(C) CITY: ROCKVILLE
(D) STATE: MD
(E) COUNTRY: US
(F) ZIP: 20850

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE: 28-JAN-1997
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: BROOKES, ANDERS A
(B) REGISTRATION NUMBER: 36,373
(C) REFERENCE/DOCKET NUMBER: PF355

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (301) 309-8504
(B) TELEFAX: (301) 309-8512

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

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47 (A) LENGTH: 2152 base pairs
48 (B) TYPE: nucleic acid
49 (C) STRANDEDNESS: single
50 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 19..1422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

63	TTCGGGCACG AGGGCAGG ATG GCG CCA CCA CCA GCT AGA GTA CAT CTA GGT																51
64	Met Ala Pro Pro Pro Ala Arg Val His Leu Gly																
65	1 5 10																
66																	
67	GCG	TTC	CTG	GCA	GTG	ACT	CCG	AAT	CCC	GGG	AGC	GCA	GCG	AGT	GGG	ACA	99
68	Ala	Phe	Leu	Ala	Val	Thr	Pro	Asn	Pro	Gly	Ser	Ala	Ala	Ser	Gly	Thr	
69	15 20 25																
70																	
71	GAG	GCA	GCC	GCG	GCC	ACA	CCC	AGC	AAA	GTG	TGG	GGC	TCT	TCC	GCG	GGG	147
72	Glu	Ala	Ala	Ala	Ala	Thr	Pro	Ser	Lys	Val	Trp	Gly	Ser	Ser	Ala	Gly	
73	30 35 40																
74																	
75	AGG	ATT	GAA	CCA	CGA	GGC	GGG	GGC	CGA	GGA	GCG	CTC	CCT	ACC	TCC	ATG	195
76	Arg	Ile	Glu	Pro	Arg	Gly	Gly	Gly	Arg	Gly	Ala	Leu	Pro	Thr	Ser	Met	
77	45 50 55																
78																	
79	GGA	CAG	CAC	GGA	CCC	AGT	GCC	CGG	GCC	CGG	GCA	GGG	CGC	GCC	CCA	GGA	243
80	Gly	Gln	His	Gly	Pro	Ser	Ala	Arg	Ala	Arg	Ala	Gly	Arg	Ala	Pro	Gly	
81	60 65 70 75																
82																	
83	CCC	AGG	CCG	GCG	CGG	GAA	GCC	AGC	CCT	CGG	CTC	CGG	GTC	CAC	AAG	ACC	291
84	Pro	Arg	Pro	Ala	Arg	Glu	Ala	Ser	Pro	Arg	Leu	Arg	Val	His	Lys	Thr	
85	80 85 90																
86																	
87	TTC	AAG	TTT	GTC	GTC	GTC	GGG	GTC	CTG	CTG	CAG	GTC	GTA	CCT	AGC	TCA	339
88	Phe	Lys	Phe	Val	Val	Val	Gly	Val	Leu	Leu	Gln	Val	Val	Pro	Ser	Ser	
89	95 100 105																
90																	
91	GCT	GCA	ACC	ATC	AAA	CTT	CAT	GAT	CAA	TCA	ATT	GGC	ACA	CAG	CAA	TGG	387
92	Ala	Ala	Thr	Ile	Lys	Leu	His	Asp	Gln	Ser	Ile	Gly	Thr	Gln	Gln	Trp	
93	110 115 120																
94																	
95	GAA	CAT	AGC	CCT	TTG	GGA	GAG	TTG	TGT	CCA	CCA	GGA	TCT	CAT	AGA	TCA	435
96	Glu	His	Ser	Pro	Leu	Gly	Glu	Leu	Cys	Pro	Pro	Gly	Ser	His	Arg	Ser	
97	125 130 135																
98																	
99	GAA	CGT	CCT	GGA	GCC	TGT	AAC	CGG	TGC	ACA	GAG	GGT	GTG	GGT	TAC	ACC	483

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100	Glu Arg Pro Gly Ala Cys Asn Arg Cys Thr Glu Gly Val Gly Tyr Thr	
101	140 145 150 155	
102		
103	AAT GCT TCC AAC AAT TTG TTT GCT TGC CTC CCA TGT ACA GCT TGT AAA	531
104	Asn Ala Ser Asn Asn Leu Phe Ala Cys Leu Pro Cys Thr Ala Cys Lys	
105	160 165 170	
106		
107	TCA GAT GAA GAA GAG AGA AGT CCC TGC ACC ACG ACC AGG AAC ACA GCA	579
108	Ser Asp Glu Glu Glu Arg Ser Pro Cys Thr Thr Thr Arg Asn Thr Ala	
109	175 180 185	
110		
111	TGT CAG TGC AAA CCA GGA ACT TTC CGG AAT GAC AAT TCT GCT GAG ATG	627
112	Cys Gln Cys Lys Pro Gly Thr Phe Arg Asn Asp Asn Ser Ala Glu Met	
113	190 195 200	
114		
115	TGC CGG AAG TGC AGC ACA GGG TGC CCC AGA GGG ATG GTC AAG GTC AAG	675
116	Cys Arg Lys Cys Ser Thr Gly Cys Pro Arg Gly Met Val Lys Val Lys	
117	205 210 215	
118		
119	GAT TGT ACG CCC TGG AGT GAC ATC GAG TGT GTC CAC AAA GAA TCA GGC	723
120	Asp Cys Thr Pro Trp Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly	
121	220 225 230 235	
122		
123	AAT GGA CAT AAT ATA TGG GTG ATT TTG GTT GTG ACT TTG GTT GTT CCG	771
124	Asn Gly His Asn Ile Trp Val Ile Leu Val Val Thr Leu Val Val Pro	
125	240 245 250	
126		
127	TTG CTG TTG GTG GCT GTG CTG ATT GTC TGT TGT TGC ATC GGC TCA GGT	819
128	Leu Leu Leu Val Ala Val Leu Ile Val Cys Cys Cys Ile Gly Ser Gly	
129	255 260 265	
130		
131	TGT GGA GGG GAC CCC AAG TGC ATG GAC AGG GTG TGT TTC TGG CGC TTG	867
132	Cys Gly Gly Asp Pro Lys Cys Met Asp Arg Val Cys Phe Trp Arg Leu	
133	270 275 280	
134		
135	GGT CTC CTA CGA GGG CCT GGG GCT GAG GAC AAT GCT CAC AAC GAG ATT	915
136	Gly Leu Leu Arg Gly Pro Gly Ala Glu Asp Asn Ala His Asn Glu Ile	
137	285 290 295	
138		
139	CTG AGC AAC GCA GAC TCG CTG TCC ACT TTC GTC TCT GAG CAG CAA ATG	963
140	Leu Ser Asn Ala Asp Ser Leu Ser Thr Phe Val Ser Glu Gln Gln Met	
141	300 305 310 315	
142		
143	GAA AGC CAG GAG CCG GCA GAT TTG ACA GGT GTC ACT GTA CAG TCC CCA	1011
144	Glu Ser Gln Glu Pro Ala Asp Leu Thr Gly Val Thr Val Gln Ser Pro	
145	320 325 330	
146		
147	GGG GAG GCA CAG TGT CTG CTG GGA CCG GCA GAA GCT GAA GGG TCT CAG	1059
148	Gly Glu Ala Gln Cys Leu Leu Gly Pro Ala Glu Ala Glu Gly Ser Gln	
149	335 340 345	
150		
151	AGG AGG AGG CTG CTG GTT CCA GCA AAT GGT GCT GAC CCC ACT GAG ACT	1107
152	Arg Arg Arg Leu Leu Val Pro Ala Asn Gly Ala Asp Pro Thr Glu Thr	

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153	350	355	360	
154				
155	CTG ATG CTG TTC TTT GAC AAG TTT GCA AAC ATC GTG CCC TTT GAC TCC			1155
156	Leu Met Leu Phe Phe Asp Lys Phe Ala Asn Ile Val Pro Phe Asp Ser			
157	365	370	375	
158				
159	TGG GAC CAG CTC ATG AGG CAG CTG GAC CTC ACG AAA AAT GAG ATC GAT			1203
160	Trp Asp Gln Leu Met Arg Gln Leu Asp Leu Thr Lys Asn Glu Ile Asp			
161	380	385	390	395
162				
163	GTG GTC AGA GCT GGT ACA GCA GGC CCA GGG GAT GCC TTG TAT GCA ATG			1251
164	Val Val Arg Ala Gly Thr Ala Gly Pro Gly Asp Ala Leu Tyr Ala Met			
165	400	405	410	
166				
167	CTG ATG AAA TGG GTC AAC AAA ACT GGA CGG AAC GCC TCG ATC CAC ACC			1299
168	Leu Met Lys Trp Val Asn Lys Thr Gly Arg Asn Ala Ser Ile His Thr			
169	415	420	425	
170				
171	CTG CTG GAT GCC TTG GAG AGG ATG GAA GAG AGA CAT GCA AAA GAG AAG			1347
172	Leu Leu Asp Ala Leu Glu Arg Met Glu Glu Arg His Ala Lys Glu Lys			
173	430	435	440	
174				
175	ATT CAG GAC CTC TTG GTG GAC TCT GGA AAG TTC ATC TAC TTA GAA GAT			1395
176	Ile Gln Asp Leu Leu Val Asp Ser Gly Lys Phe Ile Tyr Leu Glu Asp			
177	445	450	455	
178				
179	GGC ACA GGC TCT GCC GTG TCC TTG GAG TGAAAGACTC TTTTACCAG			1442
180	Gly Thr Gly Ser Ala Val Ser Leu Glu			
181	460	465		
182				
183	AGGTTTCCTC TTAGGTGTTA GGAGTTAATA CATATTAGGT TTTTTTTTTT TTTAACATGT			1502
184				
185	ATACAAAGTA AATTCTTAGC CACGTGTATT GGCTCCTGCC TGTAATCCCA TCACTTTGGG			1562
186				
187	AGGCTGACGC CGGTGGATCC ACTTGAGGTC CGAAGTTCCA AGACCAGCCC TGAACCAACA			1622
188				
189	TCGTGGAAAT GCCCGTCTTT TACAAAAAAA TACCAAAAAT TCAACTGGAA TGTGCATGGT			1682
190				
191	GTGTGCCATC ATTCCTCGG CTAACACGG GAGGTCTGAG GCCAGGAGAA TCCACTTGAA			1742
192				
193	CCCCACGAAG GACAGTGTAG ACTGCAGATT GCACCACTGC ACTCCCAGCC TGGGAACACA			1802
194				
195	GAGCAAGACT CTGTCTCAAG ATAAAATAAA ATAACTTGA AAGAATTATT GCCCGACTGA			1862
196				
197	GGCTCACATG CCAAAGGAAA ATCTGGTTCT CCCCTGAGCT GGCCTCCGTG TGTTTCCTTA			1922
198				
199	TCATGGTGGT CAATTGGAGG TGTTAATTTG AATGGATTAA GGAACACCTA GAACACTGGT			1982
200				
201	AAGGCATTAT TTCTGGGACA TTATTTCTGG GCATGTCTTC GAGGGTGTTT CCAGAGGGGA			2042
202				
203	TTGGCATGCG ATCGGGTGGG CTGAGTGGAA AAGACCTACC CTTAATTTGG GGGGGCACCG			2102
204				
205	TCCGACAGAC TGGGGAGCAA GATAGAAGAA AACAAAAAAA AAAAAAAA			2152

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206

207

208 (2) INFORMATION FOR SEQ ID NO:2:

209

210 (i) SEQUENCE CHARACTERISTICS:

211 (A) LENGTH: 468 amino acids

212 (B) TYPE: amino acid

213 (D) TOPOLOGY: linear

214

215 (ii) MOLECULE TYPE: protein

216

217 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

218

219 Met Ala Pro Pro Pro Ala Arg Val His Leu Gly Ala Phe Leu Ala Val

220 1 5 10 15

221

222 Thr Pro Asn Pro Gly Ser Ala Ala Ser Gly Thr Glu Ala Ala Ala Ala

223 20 25 30

224

225 Thr Pro Ser Lys Val Trp Gly Ser Ser Ala Gly Arg Ile Glu Pro Arg

226 35 40 45

227

228 Gly Gly Gly Arg Gly Ala Leu Pro Thr Ser Met Gly Gln His Gly Pro

229 50 55 60

230

231 Ser Ala Arg Ala Arg Ala Gly Arg Ala Pro Gly Pro Arg Pro Ala Arg

232 65 70 75 80

233

234 Glu Ala Ser Pro Arg Leu Arg Val His Lys Thr Phe Lys Phe Val Val

235 85 90 95

236

237 Val Gly Val Leu Leu Gln Val Val Pro Ser Ser Ala Ala Thr Ile Lys

238 100 105 110

239

240 Leu His Asp Gln Ser Ile Gly Thr Gln Gln Trp Glu His Ser Pro Leu

241 115 120 125

242

243 Gly Glu Leu Cys Pro Pro Gly Ser His Arg Ser Glu Arg Pro Gly Ala

244 130 135 140

245

246 Cys Asn Arg Cys Thr Glu Gly Val Gly Tyr Thr Asn Ala Ser Asn Asn

247 145 150 155 160

248

249 Leu Phe Ala Cys Leu Pro Cys Thr Ala Cys Lys Ser Asp Glu Glu Glu

250 165 170 175

251

252 Arg Ser Pro Cys Thr Thr Thr Arg Asn Thr Ala Cys Gln Cys Lys Pro

253 180 185 190

254

255 Gly Thr Phe Arg Asn Asp Asn Ser Ala Glu Met Cys Arg Lys Cys Ser

256 195 200 205

257

258 Thr Gly Cys Pro Arg Gly Met Val Lys Val Lys Asp Cys Thr Pro Trp

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/013,895

DATE: 02/25/98
TIME: 13:56:42

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Line	Error	Original Text
30	Wrong application Serial Number	(A) APPLICATION NUMBER: US

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